

GenCore version 5.1.8

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OM protein - protein search, using sw model

Run on: May 26, 2006, 21:51:38 ; Search time 182 Seconds
 (without alignments)
 763.541 Million cell updates/sec

Title: US-09-935-727-2
 Perfect score: 1634
 Sequence: 1 MRALEGPGLSLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA Main:*
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	1634	100.0	300	3	US-09-896-096A-1	Sequence 1, Appli	
2	1634	100.0	300	3	US-09-894-924-1	Sequence 1, Appli	
3	1634	100.0	300	3	US-09-935-727-2	Sequence 2, Appli	
4	1634	100.0	300	4	US-10-129-709-3	Sequence 3, Appli	
5	1634	100.0	300	4	US-10-125-985-2	Sequence 2, Appli	
6	1634	100.0	300	4	US-10-310-793-6	Sequence 6, Appli	
7	1634	100.0	300	4	US-10-369-300-19	Sequence 19, Appl	
8	1634	100.0	300	4	US-10-375-680-52	Sequence 52, Appl	
9	1634	100.0	300	4	US-10-418-242-2	Sequence 2, Appli	
10	1634	100.0	300	4	US-10-456-819-1	Sequence 1, Appli	
11	1634	100.0	300	4	US-10-793-269-2	Sequence 2, Appli	
12	1634	100.0	300	4	US-10-688-132-1	Sequence 1, Appli	
13	1634	100.0	300	4	US-10-466-786-3	Sequence 3, Appli	
14	1634	100.0	300	5	US-10-871-907-1	Sequence 1, Appli	
15	1634	100.0	300	5	US-10-775-180-145	Sequence 145, App	
16	1634	100.0	300	5	US-10-775-180-151	Sequence 151, App	

17	1634	100.0	300	5	US-10-775-180-157	Sequence 157, App
18	1634	100.0	300	5	US-10-775-180-158	Sequence 158, App
19	1634	100.0	300	5	US-10-943-197-49	Sequence 49, Appl
20	1634	100.0	300	5	US-10-775-204-439	Sequence 439, App
21	1634	100.0	300	5	US-10-775-204-452	Sequence 452, App
22	1634	100.0	300	5	US-10-775-204-491	Sequence 491, App
23	1634	100.0	300	5	US-10-775-204-494	Sequence 494, App
24	1634	100.0	300	6	US-11-154-257-2	Sequence 2, Appli
25	1634	100.0	341	4	US-10-106-698-4514	Sequence 4514, Ap
26	1634	100.0	885	5	US-10-775-180-88	Sequence 88, Appl
27	1634	100.0	885	5	US-10-775-180-89	Sequence 89, Appl
28	1634	100.0	885	5	US-10-775-204-275	Sequence 275, App
29	1634	100.0	885	5	US-10-775-204-278	Sequence 278, App
30	1634	100.0	887	5	US-10-775-180-76	Sequence 76, Appl
31	1634	100.0	887	5	US-10-775-204-223	Sequence 223, App
32	1619.5	99.1	299	3	US-09-877-156-17	Sequence 17, Appl
33	1619	99.1	300	4	US-10-793-269-4	Sequence 4, Appli
34	1612	98.7	300	3	US-09-840-795-2	Sequence 2, Appli
35	1532	93.8	326	4	US-10-264-049-3112	Sequence 3112, Ap
36	1499	91.7	879	5	US-10-775-180-77	Sequence 77, Appl
37	1499	91.7	879	5	US-10-775-204-224	Sequence 224, App
38	1492.5	91.3	880	5	US-10-775-180-70	Sequence 70, Appl
39	1492.5	91.3	880	5	US-10-775-180-74	Sequence 74, Appl
40	1492.5	91.3	880	5	US-10-775-180-87	Sequence 87, Appl
41	1492.5	91.3	880	5	US-10-775-180-90	Sequence 90, Appl
42	1492.5	91.3	880	5	US-10-775-204-217	Sequence 217, App
43	1492.5	91.3	880	5	US-10-775-204-221	Sequence 221, App
44	1492.5	91.3	880	5	US-10-775-204-274	Sequence 274, App
45	1492.5	91.3	880	5	US-10-775-204-279	Sequence 279, App

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OM protein - protein search, using sw model

Run on: May 26, 2006, 21:51:57 ; Search time 14 Seconds
 (without alignments)
 238.657 Million cell updates/sec

Title: US-09-935-727-2
 Perfect score: 1634
 Sequence: 1 MRALEGPGLSLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_New:*
 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	351.5	21.5	461	6	US-10-511-937-2945	Sequence 2945, Ap
2	351.5	21.5	461	7	US-11-183-218-32	Sequence 32, Appl
3	287	17.6	655	6	US-10-505-928-843	Sequence 843, App
4	287	17.6	655	6	US-10-196-749-418	Sequence 418, App
5	226	13.8	277	6	US-10-511-937-2455	Sequence 2455, Ap
6	211	12.9	197	7	US-11-211-917-139	Sequence 139, App
7	211	12.9	277	6	US-10-511-937-2518	Sequence 2518, Ap
8	176.5	10.8	250	7	US-11-320-192-10	Sequence 10, Appl
9	175.5	10.7	250	7	US-11-320-192-7	Sequence 7, Appli
10	170	10.4	250	7	US-11-320-192-11	Sequence 11, Appl
11	168	10.3	251	7	US-11-320-192-8	Sequence 8, Appli
12	164	10.0	243	7	US-11-320-192-12	Sequence 12, Appl
13	163	10.0	243	7	US-11-320-192-9	Sequence 9, Appli
14	155.5	9.5	260	6	US-10-511-937-2519	Sequence 2519, Ap

15	147	9.0	153	7	US-11-211-917-140	Sequence 140, App
16	134	8.2	468	6	US-10-511-937-2595	Sequence 2595, Ap
17	131	8.0	440	7	US-11-254-182-49	Sequence 49, Appl
18	128.5	7.9	417	6	US-10-505-928-793	Sequence 793, App
19	125.5	7.7	1255	6	US-10-538-066-364	Sequence 364, App
20	125.5	7.7	1255	7	US-11-223-945-43	Sequence 43, Appl
21	122	7.5	411	7	US-11-254-182-47	Sequence 47, Appl
22	119.5	7.3	236	7	US-11-293-697-4829	Sequence 4829, Ap
23	119.5	7.3	5738	6	US-10-505-928-150	Sequence 150, App
24	111	6.8	4391	7	US-11-183-325-56	Sequence 56, Appl
25	109.5	6.7	111	7	US-11-211-917-141	Sequence 141, App
26	108.5	6.6	1645	6	US-10-505-928-582	Sequence 582, App
27	107	6.5	578	6	US-10-953-349-5052	Sequence 5052, Ap
28	107	6.5	597	6	US-10-953-349-5051	Sequence 5051, Ap
29	107	6.5	631	6	US-10-953-349-5050	Sequence 5050, Ap
30	105	6.4	1193	6	US-10-505-928-537	Sequence 537, App
31	103.5	6.3	404	7	US-11-251-465-23	Sequence 23, Appl
32	103.5	6.3	969	6	US-10-505-928-94	Sequence 94, Appl
33	99.5	6.1	1259	7	US-11-223-945-40	Sequence 40, Appl
34	99.5	6.1	1308	7	US-11-248-122-2	Sequence 2, Appli
35	99	6.1	1821	6	US-10-505-928-451	Sequence 451, App
36	94.5	5.8	605	6	US-10-953-349-32398	Sequence 32398, A
37	93.5	5.7	417	6	US-10-196-749-474	Sequence 474, App
38	93.5	5.7	439	7	US-11-293-697-2765	Sequence 2765, Ap
39	92.5	5.7	633	6	US-10-953-349-10985	Sequence 10985, A
40	92.5	5.7	686	6	US-10-953-349-10984	Sequence 10984, A
41	92.5	5.7	719	6	US-10-953-349-10983	Sequence 10983, A
42	91.5	5.6	222	6	US-10-953-349-30237	Sequence 30237, A
43	91.5	5.6	724	7	US-11-293-697-3263	Sequence 3263, Ap
44	91	5.6	571	7	US-11-293-697-3307	Sequence 3307, Ap
45	91	5.6	632	6	US-10-505-928-377	Sequence 377, App

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OM protein - protein search, using sw model

Run on: May 26, 2006, 21:40:29 ; Search time 27 Seconds
 (without alignments)
 972.563 Million cell updates/sec

Title: US-09-935-727-2
 Perfect score: 1634
 Sequence: 1 MRALEGPGLSLLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1634	100.0	300	1	US-08-794-796-2	Sequence 2, Appli
2	1634	100.0	300	2	US-09-632-277A-2	Sequence 2, Appli
3	1634	100.0	300	2	US-09-523-323-52	Sequence 52, Appl
4	1634	100.0	300	2	US-09-896-096A-1	Sequence 1, Appli
5	1634	100.0	300	2	US-09-936-019-3	Sequence 3, Appli
6	1634	100.0	300	2	US-09-936-024-3	Sequence 3, Appli
7	1634	100.0	333	2	US-09-949-016-7678	Sequence 7678, Ap
8	1619.5	99.1	299	2	US-09-286-529-17	Sequence 17, Appl
9	1491	91.2	271	2	US-09-936-019-1	Sequence 1, Appli
10	1491	91.2	271	2	US-09-936-024-1	Sequence 1, Appli
11	1177	72.0	211	2	US-09-286-529-20	Sequence 20, Appl
12	855	52.3	146	2	US-09-523-323-59	Sequence 59, Appl
13	841	51.5	153	2	US-09-286-529-2	Sequence 2, Appli
14	465.5	28.5	326	2	US-10-232-858-71	Sequence 71, Appl
15	465.5	28.5	326	2	US-09-338-063A-71	Sequence 71, Appl

16	447	27.4	401	2	US-10-232-858-62	Sequence 62, Appl
17	447	27.4	401	2	US-09-338-063A-62	Sequence 62, Appl
18	445	27.2	272	2	US-10-232-858-75	Sequence 75, Appl
19	445	27.2	272	2	US-09-338-063A-75	Sequence 75, Appl
20	445	27.2	321	2	US-10-232-858-80	Sequence 80, Appl
21	445	27.2	321	2	US-09-338-063A-80	Sequence 80, Appl
22	445	27.2	327	2	US-10-232-858-72	Sequence 72, Appl
23	445	27.2	327	2	US-09-338-063A-72	Sequence 72, Appl
24	445	27.2	351	2	US-10-232-858-74	Sequence 74, Appl
25	445	27.2	351	2	US-09-338-063A-74	Sequence 74, Appl
26	445	27.2	393	2	US-10-232-858-79	Sequence 79, Appl
27	445	27.2	393	2	US-09-338-063A-79	Sequence 79, Appl
28	445	27.2	399	2	US-10-232-858-73	Sequence 73, Appl
29	445	27.2	399	2	US-09-338-063A-73	Sequence 73, Appl
30	445	27.2	401	2	US-10-232-858-5	Sequence 5, Appli
31	445	27.2	401	2	US-10-232-858-64	Sequence 64, Appl
32	445	27.2	401	2	US-10-232-858-65	Sequence 65, Appl
33	445	27.2	401	2	US-10-232-858-66	Sequence 66, Appl
34	445	27.2	401	2	US-09-338-063A-5	Sequence 5, Appli
35	445	27.2	401	2	US-09-338-063A-64	Sequence 64, Appl
36	445	27.2	401	2	US-09-338-063A-65	Sequence 65, Appl
37	445	27.2	401	2	US-09-338-063A-66	Sequence 66, Appl
38	444	27.2	293	2	US-09-896-096A-18	Sequence 18, Appl
39	444	27.2	362	2	US-10-232-858-11	Sequence 11, Appl
40	444	27.2	362	2	US-09-338-063A-11	Sequence 11, Appl
41	444	27.2	401	2	US-08-974-022-6	Sequence 6, Appli
42	444	27.2	401	2	US-09-042-785A-12	Sequence 12, Appl
43	444	27.2	401	2	US-08-795-445A-6	Sequence 6, Appli
44	444	27.2	401	2	US-08-795-447A-6	Sequence 6, Appli
45	444	27.2	401	2	US-08-974-186-6	Sequence 6, Appli